

OIPE

RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/023,673

DATE: 01/15/2002

TIME: 18:10:21

Input Set : A:\seq_listing.txt

Output Set: N:\CRF3\01152002\J023673.raw

ENTERED

```

4 <110> APPLICANT: Chen, Hong
5      Silos-Santiago, Immaculada
7 <120> TITLE OF INVENTION: NI69, A Novel Nucleoside Transporter
8      Family Member And Uses Therefor
12 <130> FILE REFERENCE: MPI2000-433CP1(M)
C--> 14 <140> CURRENT APPLICATION NUMBER: US/10/023,673
C--> 14 <141> CURRENT FILING DATE: 2001-12-17
14 <150> PRIOR APPLICATION NUMBER: 09/712797
15 <151> PRIOR FILING DATE: 2000-11-14
17 <160> NUMBER OF SEQ ID NOS: 3
19 <170> SOFTWARE: FastSEQ for Windows Version 4.0
21 <210> SEQ ID NO: 1
22 <211> LENGTH: 2625
23 <212> TYPE: DNA
24 <213> ORGANISM: Human
26 <220> FEATURE:
27 <221> NAME/KEY: 3'UTR
28 <222> LOCATION: (1)...(52)
30 <221> NAME/KEY: CDS
31 <222> LOCATION: (53)...(1477)
33 <221> NAME/KEY: 5'UTR
34 <222> LOCATION: (1478)...(2625)
36 <400> SEQUENCE: 1
37 gtcgacccac gcgtccgctt agaaggagca caggaaagtc ccagaggetg cc atg ggc 58
38                                     Met Gly
39                                     1
41 tcc gtg ggg agc cag cgc ctt gag gag ccc agc gtg gca ggc aca cca 106
42 Ser Val Gly Ser Gln Arg Leu Glu Glu Pro Ser Val Ala Gly Thr Pro
43      5                                10                                15
45 gac ccg ggc gta gtg atg agc ttc ctg ctg cca tac aac agc ttc atc 154
46 Asp Pro Gly Val Val Met Ser Phe Leu Leu Pro Tyr Asn Ser Phe Ile
47      20                                25                                30
49 acg gac gtg gac tac ctg cat cac aag tac cca ggg acc tcc atc gtg 202
50 Thr Asp Val Asp Tyr Leu His His Lys Tyr Pro Gly Thr Ser Ile Val
51 35                                40                                45                                50
53 ttt qac atg agc ctc acc tac atc ttg gtg gca ctg gca gct gtc ctc 250
54 Phe Asp Met Ser Leu Thr Tyr Ile Leu Val Ala Leu Ala Ala Val Leu
55      55                                60                                65
57 ctg aac aac gtc ctg gtg gag aga ctg acc ctg cac acc agg atc acc 298
58 Leu Asn Asn Val Leu Val Glu Arg Leu Thr Leu His Thr Arg Ile Thr
59      70                                75                                80
61 gca ggc tac ctc tta gcc ttg ggc cct ctc ctt ttt atc agc atc tgc 346
62 Ala Gly Tyr Leu Leu Ala Leu Gly Pro Leu Leu Phe Ile Ser Ile Cys
63      85                                90                                95
65 gac gtg tgg ctg cag ctc ttc tct cgg gac cag gcc tac gcc atc aac 394
66 Asp Val Trp Leu Gln Leu Phe Ser Arg Asp Gln Ala Tyr Ala Ile Asn
67      100                                105                                110

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69 ctg gcc gct gtg ggc acc gtg gcc ttc ggc tgc aca gtg cag caa tcc 442
70 Leu Ala Ala Val Gly Thr Val Ala Phe Gly Cys Thr Val Gln Gln Ser
71 115 120 125 130
73 agc ttc tac ggg tac acg gag atg ctg ccc aag cgg tac acg cag ggg 490
74 Ser Phe Tyr Gly Tyr Thr Gly Met Leu Pro Lys Arg Tyr Thr Gln Gly
75 135 140 145
77 gtg atg acc ggg gag agc acg gcg ggc gtg atg atc tct ctg agc cgc 538
78 Val Met Thr Gly Glu Ser Thr Ala Gly Val Met Ile Ser Leu Ser Arg
79 150 155 160
81 atc ctc acg aag ctg ctg ctg ccc gac gag cgc gcc agc acg ctc atc 586
82 Ile Leu Thr Lys Leu Leu Leu Pro Asp Glu Arg Ala Ser Thr Leu Ile
83 165 170 175
85 ttc ttc ctg gtg tgc gtg gcg ctg gag ctg ctg tgt ttc ctg ctg cac 634
86 Phe Phe Leu Val Ser Val Ala Leu Glu Leu Leu Cys Phe Leu Leu His
87 180 185 190
89 ctg tta gtg cgg cgc agc cgc ttc gtg ctc ttc tat acc aca cgg cgg 682
90 Leu Leu Val Arg Arg Ser Arg Phe Val Leu Phe Tyr Thr Thr Arg Pro
91 195 200 205 210
93 cgt gac agc cac cgg ggc agg cca ggc ctg ggc agg ggc tat ggc tac 730
94 Arg Asp Ser His Arg Gly Arg Pro Gly Leu Gly Arg Gly Tyr Gly Tyr
95 215 220 225
97 cgc gtg cac cac gac gtt gtc gcc ggg gac gtc cac ttc gag cac cca 778
98 Arg Val His His Asp Val Val Ala Gly Asp Val His Phe Glu His Pro
99 230 235 240
101 gcc ccg gcc ctg gcc ccc aac gag tcc cca aag gac agc cca gcc cac 826
102 Ala Pro Ala Leu Ala Pro Asn Glu Ser Pro Lys Asp Ser Pro Ala His
103 245 250 255
105 gag gtg acc ggc agc ggc ggg gcc tac atg cgc ttt gac gtg ccg cgg 874
106 Glu Val Thr Gly Ser Gly Gly Ala Tyr Met Arg Phe Asp Val Pro Arg
107 260 265 270
109 cca agg gtc cag cgc agc tgg ccc acc ttc aga gcc ctg tta ctg cac 922
110 Pro Arg Val Gln Arg Ser Trp Pro Thr Phe Arg Ala Leu Leu Leu His
111 275 280 285 290
113 cgc tac gtg gtg gcg cgg gtg atc tgg gcc gac atg ctc tcc atc gcc 970
114 Arg Tyr Val Val Ala Arg Val Ile Trp Ala Asp Met Leu Ser Ile Ala
115 295 300 305
117 gtg acc tac ttc atc acg ctg tgc ctg ttc ccc ggc ctc gag tct gag 1018
118 Val Thr Tyr Phe Ile Thr Leu Cys Leu Phe Pro Gly Leu Glu Ser Glu
119 310 315 320
121 atc cgc cac tgc atc ctg ggc gag tgg ctg ccc atc ctc atc atg gct 1066
122 Ile Arg His Cys Ile Leu Gly Glu Trp Leu Pro Ile Leu Ile Met Ala
123 325 330 335
125 gtg ttc aac ctg tca gac ttc gtg ggc aag atc ctg gca gcc ctg ccc 1114
126 Val Phe Asn Leu Ser Asp Phe Val Gly Lys Ile Leu Ala Ala Leu Pro
127 340 345 350
129 gtg gac tgg cgg ggc acc cac ctg ctg gcc tgc tcc tgc ctg cgt gtg 1162
130 Val Asp Trp Arg Gly Thr His Leu Leu Ala Cys Ser Cys Leu Arg Val
131 355 360 365 370
133 gtc ttc atc ccc ctc ttc atc ctg tgc gtc tac ccc agc ggc atg ccc 1210

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```

134 Val Phe Ile Pro Leu Phe Ile Leu Cys Val Tyr Pro Ser Gly Met Pro
135          375          380          385
137 gcc ctc cgt cac ccc gcc tgg ccc tgc atc ttc tca ctg ctc atg gcc 1258
138 Ala Leu Arg His Pro Ala Trp Pro Cys Ile Phe Ser Leu Leu Met Gly
139          390          395          400
141 atc agc aac gcc tac ttc gcc agc gtg ccc atg atc ctg gag gca gcc 1306
142 Ile Ser Asn Gly Tyr Phe Gly Ser Val Pro Met Ile Leu Ala Ala Gly
143          405          410          415
145 aaa gtg agc ccc aag cag cgg gag ctg gca ggg aac acc atg acc gtg 1354
146 Lys Val Ser Pro Lys Gln Arg Glu Leu Ala Gly Asn Thr Met Thr Val
147          420          425          430
149 tcc tac atg tca ggg ctg acg ctg ggg tcc gcc gtg gcc tac tgc acc 1402
150 Ser Tyr Met Ser Gly Leu Thr Leu Gly Ser Ala Val Ala Tyr Cys Thr
151 435          440          445          450
153 tac agc ctc acc cgc gac gct cac gcc agc tgc ctg cac gcc tcc acc 1450
154 Tyr Ser Leu Thr Arg Asp Ala His Gly Ser Cys Leu His Ala Ser Thr
155          455          460          465
157 gcc aat ggt tcc atc ctc gca gcc ctc tgagccagcc ccgccactg 1497
158 Ala Asn Gly Ser Ile Leu Ala Gly Leu
159          470          475
161 ccaggggacgc cgaggggctg accaggggccc ccaggggctg aggggcccctc cccgtgtcccc 1557
162 acctcagtgc ctgaggggccc ctgagccctcc cccgtgtgcca gcagcccccac tccctcaggg 1617
163 tccagccatg ccccaacctg gactgaagtt ctgcaaagtc ctccgaggac cggaacacgt 1677
164 ttctgcgacc cggggctctg gccagcactg tgtttctggt ttggtctcat acctgcgtct 1737
165 accttccatc tgtgtccagc ggcgccggct ccagcccagc cagcaactctg cagggtcaca 1797
166 cgcaccgtgt ccccaaccag gacagcagac acccgccaga gtgtgcgcgc ccagtgaactg 1857
167 caccgccggc ctcatcacc accggcactg atcggggca cgcctggccc agcctccacc 1917
168 agggaccctt cctcatgaac tctggagccc tgagaggaga ggggcagccc cccaccttgt 1977
169 caccctcagg gcttccccct ctgtctctcat tcttagagac tcttctccc aaacataacg 2037
170 cgttagccat gaaggagtgc gagccctggg tccgaatgga ccgcctgcg gtctgcatca 2097
171 gctctgaggc aaccacagca gtgatgccag ctgggcacgt caggacctcc ccacacccc 2157
172 acacgatgcc acaggtcagg ggctgtgcc tgactaggga gccctcccat tgccttctctg 2217
173 gcccgggata gaagagggga ggtaagtctg ggggtacga agccgggccc ccacacctg 2277
174 gctgaagtca gcttgacctt ggtcttgacc ctcatccagc aagggaactg acagacccaa 2337
175 gggtccttgg aacgtaggga ggggctgggg gtcactccag cccgggcctc ccagaacacc 2397
176 aggccctgtt gggtagccac ctgaggtcag gggatcctaa ggggtgcctt ccagagacgg 2457
177 tgtttccagg gggaggaccc cccccgttc cagatccccg gccccggctg tgactgccct 2517
178 qtttcacccc tctgtgttcc cctccccgt ctgtccacta actgtaccgc accggccatt 2577
179 aaaagatgaa ggcagaccgc tgcaaaaaaa aaaaaaaagg ggggcgcg 2625
181 <210> SEQ ID NO: 2
182 <211> LENGTH: 475
183 <212> TYPE: PRT
184 <213> ORGANISM: Human
186 <400> SEQUENCE: 2
187 Met Gly Ser Val Gly Ser Gln Arg Leu Glu Glu Pro Ser Val Ala Gly
188 1 5 10 15
189 Thr Pro Asp Pro Gly Val Val Met Ser Phe Leu Leu Pro Tyr Asn Ser
190 20 25 30
191 Phe Ile Thr Asp Val Asp Tyr Leu His His Lys Tyr Pro Gly Thr Ser

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```

192          35          40          45
193 Ile Val Phe Asp Met Ser Leu Thr Tyr Ile Leu Val Ala Leu Ala Ala
194          50          55          60
195 Val Leu Leu Asn Asn Val Leu Val Glu Arg Leu Thr Leu His Thr Arg
196 65          70          75          80
197 Ile Thr Ala Gly Tyr Leu Leu Ala Leu Gly Pro Leu Leu Phe Ile Ser
198          85          90          95
199 Ile Cys Asp Val Trp Leu Gln Leu Phe Ser Arg Asp Gln Ala Tyr Ala
200          100          105          110
201 Ile Asn Leu Ala Ala Val Gly Thr Val Ala Phe Gly Cys Thr Val Gln
202          115          120          125
203 Gln Ser Ser Phe Tyr Gly Tyr Thr Gly Met Leu Pro Lys Arg Tyr Thr
204          130          135          140
205 Gln Gly Val Met Thr Gly Glu Ser Thr Ala Gly Val Met Ile Ser Leu
206 145          150          155          160
207 Ser Arg Ile Leu Thr Lys Leu Leu Leu Pro Asp Glu Arg Ala Ser Thr
208          165          170          175
209 Leu Ile Phe Phe Leu Val Ser Val Ala Leu Glu Leu Leu Cys Phe Leu
210          180          185          190
211 Leu His Leu Leu Val Arg Arg Ser Arg Phe Val Leu Phe Tyr Thr Thr
212          195          200          205
213 Arg Pro Arg Asp Ser His Arg Gly Arg Pro Gly Leu Gly Arg Gly Tyr
214          210          215          220
215 Gly Tyr Arg Val His His Asp Val Val Ala Gly Asp Val His Phe Glu
216 225          230          235          240
217 His Pro Ala Pro Ala Leu Ala Pro Asn Glu Ser Pro Lys Asp Ser Pro
218          245          250          255
219 Ala His Glu Val Thr Gly Ser Gly Gly Ala Tyr Met Arg Phe Asp Val
220          260          265          270
221 Pro Arg Pro Arg Val Gln Arg Ser Trp Pro Thr Phe Arg Ala Leu Leu
222          275          280          285
223 Leu His Arg Tyr Val Val Ala Arg Val Ile Trp Ala Asp Met Leu Ser
224          290          295          300
225 Ile Ala Val Thr Tyr Phe Ile Thr Leu Cys Leu Phe Pro Gly Leu Glu
226 305          310          315          320
227 Ser Glu Ile Arg His Cys Ile Leu Gly Glu Trp Leu Pro Ile Leu Ile
228          325          330          335
229 Met Ala Val Phe Asn Leu Ser Asp Phe Val Gly Lys Ile Leu Ala Ala
230          340          345          350
231 Leu Pro Val Asp Trp Arg Gly Thr His Leu Leu Ala Cys Ser Cys Leu
232          355          360          365
233 Arg Val Val Phe Ile Pro Leu Phe Ile Leu Cys Val Tyr Pro Ser Gly
234          370          375          380
235 Met Pro Ala Leu Arg His Pro Ala Trp Pro Cys Ile Phe Ser Leu Leu
236 385          390          395          400
237 Met Gly Ile Ser Asn Gly Tyr Phe Gly Ser Val Pro Met Ile Leu Ala
238          405          410          415
239 Ala Gly Lys Val Ser Pro Lys Gln Arg Glu Leu Ala Gly Asn Thr Met
240          420          425          430

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```

241 Thr Val Ser Tyr Met Ser Gly Leu Thr Leu Gly Ser Ala Val Ala Tyr
242           435           440           445
243 Cys Thr Tyr Ser Leu Thr Arg Asp Ala His Gly Ser Cys Leu His Ala
244           450           455           460
245 Ser Thr Ala Asn Gly Ser Ile Leu Ala Gly Leu
246 465           470           475
249 <210> SEQ ID NO: 3
250 <211> LENGTH: 1428
251 <212> TYPE: DNA
252 <213> ORGANISM: Human
254 <220> FEATURE:
255 <221> NAME/KEY: CDS
256 <222> LOCATION: (1)...(1428)
258 <400> SEQUENCE: 3
259 atg ggc tcc gtg ggg agc cag cgc ctt gag gag ccc agc gtg gca ggc      48
260 Met Gly Ser Val Gly Ser Gln Arg Leu Glu Glu Pro Ser Val Ala Gly
261 1           5           10           15
263 aca cca gac ccg ggc gta gtg atg agc ttc ctg ctg cca tac aac agc      96
264 Thr Pro Asp Pro Gly Val Val Met Ser Phe Leu Leu Pro Tyr Asn Ser
265           20           25           30
267 ttc atc acg gac gtg gac tac ctg cat cac aag tac cca ggg acc tcc      144
268 Phe Ile Thr Asp Val Asp Tyr Leu His His Lys Tyr Pro Gly Thr Ser
269           35           40           45
271 atc gtg ttt gac atg agc ctc acc tac atc ttg gtg gca ctg gca gct      192
272 Ile Val Phe Asp Met Ser Leu Thr Tyr Ile Leu Val Ala Leu Ala Ala
273           50           55           60
275 gtc ctc ctg aac aac gtc ctg gtg gag aga ctg acc ctg cac acc agg      240
276 Val Leu Leu Asn Asn Val Leu Val Glu Arg Leu Thr Leu His Thr Arg
277 65           70           75           80
279 atc acc gca ggc tac ctc tta gcc ttg ggc cct ctc ctt ttt atc agc      288
280 Ile Thr Ala Gly Tyr Leu Leu Ala Leu Gly Pro Leu Leu Phe Ile Ser
281           85           90           95
283 atc tgc gac gtg tgg ctg cag ctc ttc tct cgg gac cag gcc tac gcc      336
284 Ile Cys Asp Val Trp Leu Gln Leu Phe Ser Arg Asp Gln Ala Tyr Ala
285           100          105          110
287 atc aac ctg gcc gct gtg ggc acc gtg gcc ttc ggc tgc aca gtg cag      384
288 Ile Asn Leu Ala Ala Val Gly Thr Val Ala Phe Gly Cys Thr Val Gln
289           115          120          125
291 caa tcc agc ttc tac ggg tac acg ggg atg ctg ccc aag cgg tac acg      432
292 Gln Ser Ser Phe Tyr Gly Tyr Thr Gly Met Leu Pro Lys Arg Tyr Thr
293           130          135          140
295 cag ggg gtg atg acc ggg gag agc acg gcg ggc gtg atg atc tct ctg      480
296 Gln Gly Val Met Thr Gly Glu Ser Thr Ala Gly Val Met Ile Ser Leu
297 145          150          155          160
299 agc cgc atc ctc acg aag ctg ctg ctg ccc gac gag cgc gcc agc acg      528
300 Ser Arg Ile Leu Thr Lys Leu Leu Leu Pro Asp Glu Arg Ala Ser Thr
301           165          170          175
303 ctc atc ttc ttc ctg gtg tcg gtg gcg ctg gag ctg ctg tgt ttc ctg      576
304 Leu Ile Phe Phe Leu Val Ser Val Ala Leu Glu Leu Leu Cys Phe Leu

```

VERIFICATION SUMMARY

PATENT APPLICATION: US/10/023,673

DATE: 01/15/2002

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Input Set : A:\seq listing.txt

Output Set: N:\CRF3\01152002\J023673.raw

L:14 M:270 C: Current Application Number differs. Replaced Current Application No

L:14 M:271 C: Current Filing Date differs. Replaced Current Filing Date